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(54) Title: NUCLEOTIDE SEQUENCES SPECIFIC TO FRANCISELLA TULARENSIS AND METHODS FOR THE DETECTION OF FRANCISELLA TULARENSIS

(57) Abstract: Described herein is the identification of nucleotide sequences specific to *Francisella tularensis* that serves as a marker or signature for identification of this bacterium. In addition, forward and reverse primers and hybridization probes derived from these nucleotide sequences that are used in nucleotide detection methods to detect the presence of the bacterium are disclosed.



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NUCLEOTIDE SEQUENCES SPECIFIC TO FRANCISELLA TULARENSIS
AND
METHODS FOR THE DETECTION OF
FRANCISELLA TULARENSIS

[0001] The United States Government has rights in this invention pursuant to Contract No. W-7405-ENG-48 between the United States Department of Energy and the University of California for the operation of Lawrence Livermore National Laboratory.

RELATED APPLICATION

[0002] This application claims the benefit of U.S. Provisional Application No. 60/400,892, filed August 1, 2002, and entitled, "DNA Diagnostics Francisella Tularensis Species," which is incorporated herein by this reference.

SEQUENCE LISTING IN COMPUTER READABLE FORM

[0003] The sequence listing information recorded in computer readable form is identical to the written on paper sequence listing.

BACKGROUND

[0004] *Francisella tularensis* is the species of bacteria known to cause what is commonly known as Tuleremia, a serious and sometimes fatal disease. Since the attack on the World Trade Center in New York of September 11, 2001, there has been a growing concern that terrorists or rogue governments will use the *Francisella tularensis* bacterium as a weapon of mass destruction and instrument of terror. Since the events of September 11, 2001, the United States Government has been developing reliable methods and systems to detect the *Francisella tularensis* bacterium so that immediate and effective counter measures can be undertaken. The existing methods for detecting the *Francisella tularensis* bacterium are considered inadequate because of the higher than acceptable rate of

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false positive and false negative results. False positive results lead to confusion regarding whether the *Francisella tularensis* bacterium is actually present and whether protective measures should immediately be implemented. Conversely, false negative results would allow the *Francisella tularensis* bacterium to remain undetected with consequent adverse impacts. A more reliable method of detecting the *Francisella tularensis* bacterium would reduce the occurrence of false positive and false negative results and provide decision makers with greater confidence in implementing appropriate counter measures.

SUMMARY OF THE INVENTION

[0005] An aspect of the invention includes the nucleotide sequences that are identified in SEQ ID NOs:4, 8, 12, 16, 20, 24, 28 and 32 that are specific to *Francisella tularensis*.

[0006] Another aspect of the invention includes a Forward Primer, the nucleotide sequences that are identified in SEQ ID NOs:1, 5, 9, 13, 17, 21, 25, and 29 and any primers that are derived from these nucleotide sequences.

[0007] A further aspect of the invention is a Reverse Primer, the nucleotide sequences that are identified in SEQ ID NOs:2, 6, 10, 14, 18, 22, 26 and 30 and any primers that are derived from these nucleotide sequences.

[0008] A further aspect of the invention is includes a Hybridization Probe, the nucleotide sequences that are identified in SEQ ID NOs:3, 7, 11, 15, 19, 23, 27 and 31 and any probes that are derived from these nucleotide sequences.

[0009] This invention also includes a method for the detection of *Francisella tularensis* using the bacterium specific nucleotide sequence comprising: providing a sample in an environment that is suitable for isolating genomic DNA for amplification using PCR and under conditions suitable for hybridization with a least one group of nucleotides consisting of forward primer, a reverse primer and a hybridization probe and detecting the existence of *Francisella Tularensis* specific nucleotide sequences by a nucleotide detection method, such as PCR and fluorescent 5' nuclease PCR assay, wherein the existence of the nucleotide sequence indicates the presence of *Francisella tularensis* in the sample.

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BRIEF DESCRIPTION OF THE SEQUENCES

SEQ ID NO:1	Primer
SEQ ID NO:2	Primer
SEQ ID NO:3	Probe
SEQ ID NO:4	Amplicon
SEQ ID NO:5	Primer
SEQ ID NO:6	Primer
SEQ ID NO:7	Probe
SEQ ID NO:8	Amplicon
SEQ ID NO:9	Primer
SEQ ID NO:10	Primer
SEQ ID NO:11	Probe
SEQ ID NO:12	Amplicon
SEQ ID NO:13	Primer
SEQ ID NO:14	Primer
SEQ ID NO:15	Probe
SEQ ID NO:16	Amplicon
SEQ ID NO:17	Primer
SEQ ID NO:18	Primer
SEQ ID NO:19	Probe
SEQ ID NO:20	Amplicon
SEQ ID NO:21	Primer
SEQ ID NO:22	Primer
SEQ ID NO:23	Probe
SEQ ID NO:24	Amplicon
SEQ ID NO:25	Primer
SEQ ID NO:26	Primer
SEQ ID NO:27	Probe

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SEQ ID NO:28	Amplicon
SEQ ID NO:29	Primer
SEQ ID NO:30	Primer
SEQ ID NO:31	Probe
SEQ ID NO:32	Amplicon

DETAILED DESCRIPTION

[00010] Disclosed herein are nucleotide sequences located on different loci of the *Francisella tularensis* bacterium genome, and primers and the hybridization probes used in detecting the specific nucleotide sequences. Also disclosed is a method for identifying *Francisella tularensis* by analyzing samples taken from monitoring devices, such as air monitors, for the nucleotide sequences that are specific to *Francisella tularensis*. As the nucleotide sequences that have been identified are unique to the *Francisella tularensis* bacterium, using the primers and hybridization probes to detect the presence of the *Francisella tularensis* bacterium is far more reliable than existing methods and partly reduces the occurrence of false positive and false negative results.

[00011] *Francisella tularensis* is the bacterium that causes Tularemia, a disease that can be fatal if not detected and treated with appropriate antibiotics. The symptoms of Tularemia “could include sudden fever, chills, headaches, muscle aches, joint pain, dry cough, progressive weakness, and pneumonia”, this information can be found at the internet address www.bt.cdc.gov/documentsapp/FactSheet/Tularemia/about.asp. It is on the Center for Disease Control and Prevention (CDC) list of possible bacteria that has potential as a biological warfare weapon. The CDC has developed a list of possible pathogens that may be used as weapons of mass destruction. *Francisella tularensis* has been listed in Category A of possible diseases and agents. Those diseases and agents in Category A are considered a high risk to national security because they “can be easily disseminated or transmitted from person to person; result in high mortality rates and have the potential for major public health

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impact; might cause public panic and social disruption; and require special action for public health preparedness”, this information can be found at the internet address www.bt.cdc.gov/agent/agentlist-category.asp.

[00012] A key element in developing defenses against the use of *Francisella tularensis* is the ability to quickly and accurately detect the presence of the bacterium. Early detection will allow for the implementation of effective counter measures. Additionally, early detection will allow for the identification and treatment of those that may have been exposed to the bacterium. Early detection and treatment is essential for the treatment of Tularemia because although the disease may be fatal, it is usually treatable with antibiotics upon early detection.

[00013] Existing detection methods have resulted in a higher than acceptable rate of false positive and false negative results. Such results are inadequate and can create confusion regarding the appropriate countermeasures, if any, that should be undertaken because it is unclear whether the bacterium is present or not. If the bacterium is not present, undertaking counter measures may cause undue expense and create unwarranted concern among those that may incorrectly believe they have been exposed.

[00014] Although the genome for *Francisella tularensis* has already been mapped, this alone is not sufficient to develop a reliable and accurate detection mechanism because the current methods use nucleotide sequences that may be common to many different bacteria. Thus, existing detection methods could not distinguish between various bacteria, which results in higher than acceptable false positive detection rates. Similarly, some existing detection methods result in false negative results because they are not sensitive enough to detect the bacterium.

[00015] Using a nucleotide sequence that is specific to results in a more reliable detection method.

[00016] In order to detect any of the eight amplicons specific to *Francisella tularensis*, a series of forward and reverse primers and hybridization probes were developed for each of the eight amplicons.

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[00017] A typical assay can determine the presence of SEQ ID Nos 4 and 8 using the sequence specific primers and the hybridization probes. If there is a positive result for the presence of *Francisella tularensis* then an assay is run to determine the presence of additional amplicon sequences, as a means to double check for the presence of *Francisella tularensis*.

[00018] Identifications of the *Francisella tularensis* specific nucleotide sequences allows the presence of the bacteria to be detected from environmental samples using PCR assay analysis and detection. PCR is a technique utilized to amplify genomic DNA. Typical PCR reactions include appropriate PCR buffers, nuclease polymerase and one or more oligonucleotide primers and hybridization probes. Various modifications of PCR techniques are possible as detailed in Current Protocols in Molecular Biology ed. F.M. Ausubel, R. Brent, D.D. Moore, K. Struhle, Massachusetts General Hospital and Harvard Medical School (1987) which is hereby incorporated by reference. The following US patents describe PCR and are incorporated herein by reference: US 4,683,195; US 4,683,202; US 4,800,159.

[00019] One method that may be used for real-time PCR amplification and detection is TaqMan®. The principles involved in the conventional Taqman® 5' exonuclease assay are described in detail by Holland et al in, *Detection of specific polymerase chain reaction product by utilizing the 5'----3' exonuclease activity of Thermus aquaticus polynucleotide polymerase*, Proc Natl Acad Sci U S A 88 (16):7276-80, 1991, which is herein incorporated by reference. TaqMan® real time detection can also be used to simultaneously detect a plurality of nucleic acid targets when it is used with multiplex PCR, which enables simultaneous detection of more than one target sequence, thus enhancing detection accuracy. A few examples of typical PCR instruments include the ABI prism 7700, the Cepheid Smart Cycler, and the Bio-Rad iCycler.

In order to use a PCR assay method for detection of the *Francisella tularensis* bacterium, the sample must be prepared to extract all DNA that may be present. The following is a protocol for the preparation of samples taken from ambient air

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monitoring devices for nucleotide detection using fluorogenic 5' nuclease PCR assay.

Assay Protocol

Definitions:

DNA-deoxyribonucleic acid

EDTA-ethylenediaminetetraacetic acid

PCR-polymerase chain reaction

PCR water-autoclaved water, then filtered

CT-cycle threshold-the cycle in which the fluorescence signal crosses a user defined

threshold

FAM-reporter dye

TAMRA-quencher dye

Sample Preparation:

[00020] Exposed environmental filters are suspended in Sodium phosphate/EDTA, Tween buffer and bead beaten. The supernatant is filtered and washed to yield the genomic DNA extract. The extract is then subjected to real-time polymerase chain reaction (PCR) assay using a fluorescent-labeled probe. This process monitors a PCR reaction and the quantity of double-stranded product that is produced

Materials Needed:

[00021] A series of forward and reverse primers, a hybridization probe and polymerase reagents specific to the first amplicon to be detected. A series of forward and reverse primers, a hybridization probe and polymerase reagents specific to the second amplicon to be detected.

Bead beater Kit with the following labeled components:

- a. 3 capped tubes containing a filter and beads
- b. 3 yellow ultra free MC Centrifugal Filter Units
- c. 6 blue microcon YM-100 filter units
- d. 12 collection tubes

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- e. 7 PCR reaction mix-includes primer/ probe and Taq-labeled A,B,C,D,E,F,G
- f. 48 –25 μ l Smart Cycle reaction tubes
- g. Sodium phosphate buffer/EDTA Teen buffer
- h. PCR water
- i. Inhibitory control DNA
- j. Extra unlabeled tubes

Materials not provided in the bead beater kit:

- a. Cepheid Smart Cycle
- b. Microcentrifuge
- c. Microfuge for Cepheid tubes

Preparation of DNA Extract:

This part of the assay protocol is performed in segregated work areas and in a biosafety cabinet using BSL 2 practices.

1. Add 400 μ l of Sodium phosphate/ED TA Teen buffer to each of the capped tubes containing a filter and beads. Screw cap tightly.
2. Insert tubes one at a time into the bead beater.
3. Bead beat the capped tube for 3 minutes and a speed of 5000 rpm.
4. Remove capped tube from bead beater and place the tube on ice for a minimum of 2 minutes to cool.
5. Wash Steps.
 - Spin capped filter tubes for 10 seconds (pulse spin) in microcentrifuge.
 - Transfer approximately 400 μ l of the supernatant to the yellow top filter collection tube.
 - Spin the yellow top filter tube with the supernatant @ 7000 rpm for 3 minutes.
 - Transfer the filtered liquid to a blue microcon filter on collection tube #1.
 - Spin @ 7000 rpm for 1 minute. Check fluid level in the blue microcon filter. If it is above the white base, pulse spin for about 10

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seconds to bring the level at or a little below the white area. It could take more than one pulse spin to bring the level down. This is approximately 100-200 μ l of liquid.

- Transfer this liquid on the top of the filter to a second blue microcon filter on a clean collection tube #2. Tilt the tube at a 45° angle and take off the liquid-do NOT vacuum the filter.
- Add 400 μ l of PCR water to the second blue microcon filter with the added liquid.
- Spin @ 7000 rpm for 2 minutes. Do not be spin dry; there should be about 50-100 μ l of liquid on top of the filter. Pulse spin if the level is too high
- Using clean, metal forceps remove the blue microcon filter from the collection tube #2 and place the blue microcon filter on a clean collection tube #3. Discard collection tube #2.
- Add 400 μ l PCR water to the blue microcon filter on collection tube #3.
- Spin @ 7000 rpm for 2 minutes. Do not be spin dry; there should be about 50-100 μ l of liquid on top of the filter. Pulse spin if the level is too high.
- Remove the blue microcon filter. Place the blue microcon filter on collection tube #4. Discard collection tube #3
- Add 400 μ l PCR water to the blue microcon filter on collection tube #4.
- Spin for 1 minute @ 7000 rpm. Check fluid level in the blue microcon filter. If it is above the white base, pulse spin for about 10 seconds to bring the level at or a little below the white area. This could take more than one pulse spin. If the level of liquid is at or a little below the white base, this is approximately 100-200 μ l of DNA extract.

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If for some reason the pulse spin has brought the level of DNA extract down too low add 200 μ l PCR water and bring the level carefully to the white base level by pulse spinning for less time).

- Transfer the liquid on the top of the blue microcon filter (your DNA extract) to the eppendorf tube.
- If you cannot perform the PCR assay immediately, keep extract refrigerated.

PCR Assay:

1. Thaw on ice each set of primer/probe/Taq polymerase sets. Once thawed PCR assay must begin. Do NOT refreeze. Keep on ice while testing.
2. Add 20 μ l of each of the PCR reaction mixes for each amplicon and one inhibitory control to the appropriately labeled Cepheid reaction tubes; e.g. 1-1A is for amplicon 1, filter 1, a set of primers, probe, Taq polymerase.
 - a. Add 5 μ l of DNA extract to each of the tubes-rinse tip 1-2 times in the mix and discard the tip.
 - b. Use a clean tip for each reaction tube.
 - c. Each tube should have a total of 25 μ l .
3. Add 15 μ l of PCR reaction inhibitory mix to appropriately labeled Cepheid tubes; e.g INHIB.
 - a. Add 5 μ l DNA extract to each tube-rinse tip 1-2 times in the mix and discard tip.
 - b. Add 5 μ l of DNA inhibitory control to each tube-rinse tip 1-2 times in the mix
nd discard the tip.
 - a. Use a clean tip for each reaction tube.
 - b. Each tube should have a total of 25 μ l .
4. Include as controls:
 - NTC (no template control) for each set of primers/probe, Taq.

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5. Spin Cepheid tubes in Cepheid microfuge for about 4 seconds. This mixes the PCR reaction mix and DNA into the optic diamond area. Check to see that the optic area is filled.

Run Cepheid Smart Cycler

Record all CT values (including 0) on the result sheet for the appropriate organism and filter.

6. CT values from 34 to 35 indicate negative readings – no *Francisella* DNA detected. CT values below 34 indicate positive readings – *Francisella* DNA detected.

[00022] Table 1 shows the results of assay runs that were performed using the above described protocol. An assay set containing the primers and probe for each amplicon sequence was added to a sample containing either the *Francisella tularensis* bacteria or *Francisella philomiragia*. The *Francisella philomiragia* bacteria is similar in genetic composition to its cousin *Francisella tularensis*. *Francisella philomiragia* was, therefore, used as a control to demonstrate that the primers and probe derived from the *Francisella tularensis* specific amplicon could distinguish between genetic near neighbors, thereby demonstrating the specificity of the amplicon sequence. Three different strains of the *philomiragia* bacteria were used, 25016, 25017 and 25018. The *Francisella tularensis* and the *Francisella philomiragia* DNA was obtained from American Type Culture Collection. The assay sets containing the probes and primers were obtained from various vendors such as ABI and Biosearch.

[00023] All assays were run three times with the exception of *Francisella philomiragia* #25018 which was run twice. The results show that the assay runs having the *Francisella tularensis* DNA in the sample had positive results, CT values of less than 34. Those assay runs having *Francisella philomiragia* in the sample had negative results, CT values of 34 to 35. These results show that the primers and probe derived from the *Francisella tularensis* specific amplicon can distinguish between near genetic neighbors of the *Francisella* bacteria, thus

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demonstrating that the nucleotide sequences in the amplicons are specific to *Francisella tularensis*.

TABLE 1

F.t. taqman probe assay

F. tularensis = NY98-09217

Sample size = 2ng

Assay Set	7700 run1 F. tularensis	7700 run2 F. tularensis	7700 run3 F. tularensis	Cepheid run1 F. tularensis	Cepheid run2 F. tularensis	Cepheid run3 F. tularensis		
ftT0416r2C136.tF: Seq. ID No. 1, 2, 3	23.14	25.87	26.07	29.32	28.45	28.52		
ftT0416r2C228.tF: Seq. ID No. 5, 6, 7	20.57	22.17	22.26	21.38	21.20	21.65		
ftT0416r2C74.tF: Seq. ID No. 9, 10, 11	19.81	20.79	20.88	20.13	21.19	20.83		
C124.tF: Seq. ID No. 13, 14, 15	19.76	20.73	20.58	19.49	20.06	19.60		
C136.tF: Seq. ID No. 17, 18, 19	20.67	21.03	21.19	20.73	22.58	20.16		
ft5698r2C106.tF: Seq. ID No. 21, 22, 23	20.1	20.52	20.36	20.34	22.06	19.68		
ft5698r2C127.tF: Seq. ID No. 25, 26, 27	20.99	22.82	23.27	21.12	22.45	20.70		
ft5698r2C86.tF: Seq. ID No. 29, 30, 31	20.9	21.57	21.57	21.28	21.52	21.23		

Assay Set	7700 run1 Philo. #25016	7700 run2 Philo. #25016	7700 run3 Philo. #25016	7700 run1 Philo. #25017	7700 run2 Philo. #25017	7700 run3 Philo. #25017	7700 run1 Philo. #25018	7700 run2 Philo. #25018
ftT0416r2C136.tF: Seq. ID No. 1, 2, 3	35	35	35	35	35	35	35	35
ftT0416r2C228.tF: Seq. ID No. 5, 6, 7	35	35	35	35	35	35	35	35
ftT0416r2C74.tF: Seq. ID No. 9, 10, 11	35	35	35	35	35	35	35	35
C124.tF: Seq. ID No. 13, 14, 15	35	35	35	35	35	35	35	35
C136.tF: Seq. ID No. 17, 18, 19	35	35	35	35	35	35	35	35
ft5698r2C106.tF: Seq. ID No. 21, 22, 23	35	35	35	35	35	35	35	35
ft5698r2C127.tF: Seq. ID No. 25, 26, 27	35	35	35	35	35	35	35	35
ft5698r2C86.tF: Seq. ID No. 29, 30, 31	35	35	35	35	35	35	35	35

[00024] The nucleotide sequences disclosed herein are specific to *Francisella tularensis*. Accordingly, although air monitors are an effective method of obtaining samples for analyses, a wide variety of other media and methods may be used to provide the samples for analysis for the *Francisella tularensis* bacterium.

[00025] All numbers expressing quantities of ingredients, constituents, reaction conditions, and so forth used in the specification and claims are to be understood as being modified in all instances by the term "about". Notwithstanding that the numerical ranges and parameters setting forth the broad scope of the subject matter presented herein are approximations, the numerical values set forth in the specific examples are reported as precisely as possible. Any numerical value, however, inherently contain certain errors necessarily resulting from the standard deviation found in their respective testing measurements.

[00026] All publications and patents mentioned in the above specification are herein incorporated by reference. Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

The invention claimed is:

1. A composition comprising an Amplicon, a single strand sequence of nucleic acids specific to *Francisella tularensis*, selected from the group consisting of SEQ ID NO:4, 8, 12, 16, 20, 24, 28 and 32.
2. A composition comprising a single strand sequence of nucleic acids that is complimentary to the sequence of nucleic acids recited in Claim 1 or any portion thereof.
3. A composition comprising a single strand sequence of nucleic acids selected from the group consisting of SEQ ID NOs:1, 2, 3, 5, 6, 7, 9, 10, 11, 13, 14, 15, 17, 18, 19, 21, 22, 23, 25, 26, 27, 29, 30 and 31.
4. A method comprising:
 - (i) providing a sample;
 - (ii) forming a mixture by adding the sample to a solution containing at least one series of nucleotide sequences having a forward primer, a reverse primer and a hybridization probe selected from the group consisting of SEQ ID NOs:1, 2, 3; 5, 6, 7; 9, 10, 11; 13, 14, 15; 17, 18, 19; 21, 22, 23; 25, 26, 27; 29, 30, 31; under conditions suitable for isolating genomic DNA for amplification using PCR and under conditions suitable for hybridization with said at least one series of nucleotide sequences; and
 - (iii) subjecting the mixture to PCR.
5. The method of Claim 4 wherein said PCR comprises standard PCR.
6. The method of Claim 5, wherein said PCR comprises fluorogenic 5' nuclease PCR assay.
7. A method comprising:
 - (i) providing a sample;
 - (ii) forming a mixture by adding the sample to a solution containing at least one series of nucleotide sequences having a forward primer, a reverse primer and a hybridization probe selected from the group consisting of SEQ ID NOs:1, 2, 3; 5, 6, 7; 9, 10, 11; 13, 14, 15; 17, 18, 19; 21, 22, 23; 25, 26, 27; 29, 30, 31; under conditions suitable for isolating genomic DNA for

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amplification using PCR and under conditions suitable for hybridization with said at least one series of nucleotide sequences; and

(iii) detecting the presence of at least one Amplicon sequence by flurogenic 5' nuclease PCR assay, wherein the presence of said one Amplicon sequence indicates the existence of *Francisella tularensis* in the sample.

GENE SEQUENCES

<110> McCready, Paula M

Radnedge, Lyndsey

Anderson, Gary L

Ott, Linda L

Slezak, Thomas R

Kuczmarski, Thomas A

Vitalis, Elizabeth A

<120> Nucleotide Sequences Specific to Francisella Tularensis and
Methods for Detection of Francisella Tularensis

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